

A Review of Literature Measuring Years of Life Lost Due to COVID-19: The Search for Comorbidity Inclusion

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Abstract

COVID-19 (corona virus disease 19), caused by SARS-CoV-2 (severe acute respiratory syndrome virus 2), is characterized by a diverse range of clinical manifestations, predominately respiratory disease. Risk factors for severe COVID-19 include old age (> 65 years of age), male sex, and pre-existing conditions (e.g., cancer, obesity, heart disease, lung disease, diabetes, etc.), among other factors. COVID-19 disproportionately impacts individuals with pre-existing conditions; therefore, it is critical that estimations of COVID-19 mortality are representative to provide targeted interventions. Years of life lost (YLL) is an important public health tool that provides public health officials, clinicians, and researchers a means to estimate the duration of life an individual may have realized had they not died prematurely. YLL measurements do not include the impact of single and multiple comorbidities on premature mortality; therefore, YLL estimations are known to be over-estimates. The purpose of this essay was to analyze COVID-19 YLL literature to assess YLL measurements and/or models which include comorbidities. The existence of a YLL model, which incorporates comorbidities, could dramatically improve health care clinicians and policymakers' capabilities to determine the impact of COVID-19 on at-risk populations. COVID-19 YLL literature that includes comorbidities is limited, however, a manuscript by authors Hanlon et al. estimated the likely combinations of comorbidities among people who have died from COVID-19 and then

estimated life expectancy based on age, sex, and the comorbidity combinations to estimate YLL. This model has the potential to enhance the understanding of factors contributing to COVID-19 mortality and implications for clinical practice, public health policy, and guidelines for COVID 19 management. The model could be improved with the inclusion of other variables, including personal-level data, additional clinical comorbidities, race, socio-economic status (SES), occupation, specific health behaviors, and institutional settings, such as nursing home status.

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List of Abbreviations

ACE2	Human Angiotensin-Converting Enzyme 2
CDC	Centers for Disease Control and Prevention
COVID-19	Corona virus disease 2019
DALY	Disability-Adjusted Life Years
LE	Life Expectancy
MERS	Middle Eastern Respiratory Syndrome
RAAS	Renin-Angiotensin-Aldosterone System
RBD	Receptor Binding Domain
SARS	Severe Acute Respiratory Syndrome
SARS-CoV-2	Severe Respiratory Syndrome Coronavirus 2
SES	Socio-Economic Status
SMR	Standard Mortality Ratio
UK	United Kingdom
WHO	World Health Organization
YLL/PYLL	Years of Life Lost/Potential Years of Life Lost

Preface

I want to sincerely thank Dr. Yassin, Dr. Frank, Heather Dixon, and Dr. Martinson. Each of you provided me guidance, mentorship, and helped me indirectly or directly throughout this entire process. I also want to thank my girlfriend for her moral support and my dog Milly, who decided she had to sit on my lap whenever I worked on my essay.

1.0 Introduction

On January 9th, 2020, the World Health Organization (WHO) announced the emergence of a novel coronavirus-related pneumonia in Wuhan China (WHO, 2020b). On January 11th, China reported its first ‘Corona virus disease 2019’ (COVID-19) death, with the first death outside of China reported on February 2nd (WHO, 2020b). By late February, international spread of the virus that causes COVID-19, ‘severe respiratory syndrome coronavirus 2’ (SARS-CoV-2), began to accelerate (WHO, 2020b).

On March 11th, 2020, the WHO declared COVID-19 a pandemic (Dos Santos, 2020; WHO, 2020a). A month later, at the end of April, the world surpassed at least 200,000 known COVID-19 deaths (CDC, 2021a). By the end of 2020, nearly 84 million cases and nearly two million deaths had been recorded, with the United States leading in both infections and deaths; 20 million infections and 346,000 deaths (CDC, 2021a).

The global spread of SARS-CoV-2 cannot be attributed to one factor, but a multitude of factors. These factors include a basic reproductive rate (R_0) greater than one (Petersen et al., 2020), pre-symptomatic and asymptomatic transmission (Cevik, Kuppalli, Kindrachuk, & Peiris, 2020; Furukawa, Brooks, & Sobel, 2020; Meyerowitz, Richterman, Gandhi, & Sax, 2021; Petersen et al., 2020), a peak viral load in the respiratory tract at time of symptom onset or in the first week of illness (Cevik et al., 2020; Petersen et al., 2020), airborne transmission, super-spreading events, and anthropological factors (e.g. global travel).

COVID-19 has not impacted all populations equally, as COVID-19 morbidity and mortality has disproportionally affected individuals aged 65 and older, individuals with pre-existing conditions, males (Atkins et al., 2020; Barnett et al., 2012; CDC, 2021b; Cevik et al., 2020; Williamson et al., 2020), and individuals in a low socio-economic class (Karmakar, Lantz, & Tipirneni, 2021; Seligman, Ferranna, & Bloom, 2021). Therefore, it is important to examine the impact of COVID-19 mortality on at-risk populations. Estimating the years of life lost (YLL), also known as potential years of life lost (PYLL), is a viable public health tool to examine pre-mature mortality from COVID-19.

As early as the 1940's, researchers sought to measure the social and economic loss resulting from premature death (Haenszel, 1950). YLL/PYLL models were developed to provide public health officials and policy makers a more appropriate metric than death counts for measuring the mortality impact of a condition on a population and sub-populations. Conventional YLL measurements use the age at death combined with life expectancy for that age, based on a national life table, to estimate the weighted average of YLL (Hanlon, 2021). YLL models function both as an indicator for setting priorities for prevention and intervention and as an approach to compare premature mortality between populations (PHAST, 2020).

It is important to highlight that YLL measurements can never truly be observed because estimating YLL requires counterfactual assumptions of how long a person would have lived if they had not died (Devleesschauwer, 2020). YLL measurements also fail to include the effect of comorbidities, especially multimorbidity. Comorbidities are likely to play a significant role in premature death; therefore, not accounting for comorbidities in YLL measurements may lead to an artificial increase of the YLL.

Given the role of multimorbidity and comorbidity in COVID-19 mortality, it would be beneficial to measure YLL, accounting for the effects of a single comorbidity or multimorbidity. Measuring YLL with the inclusion of comorbidities would produce more accurate comparisons of COVID-19's role in premature mortality between at-risk populations. This approach can also provide a more realistic approach to revising guidance and policies towards at-risk populations.

The main purpose of this essay is to review COVID-19 YLL literature to assess YLL models or measurements which include comorbidities. Such a model or measurement could provide a measurable and reliable means to determine the true impact of COVID-19 on an at-risk population or populations, thereby demonstrating the need of mitigation efforts and interventions to the public, health policy makers, and clinical leaders.

2.0 SARS-CoV-2 and COVID-19

Initial cases of COVID-19 in December of 2019, at the time reported as a pneumonia of unknown cause, were epidemiologically associated with the Huanan South China Seafood Market in Hubei province, a wet market where live and dead animals are sold (Dos Santos, 2020; Hu, Guo, Zhou, & Shi, 2021). Patients hospitalized with the ‘unknown pneumonia’ presented with symptoms similar to Severe Acute Respiratory Syndrome (SARS) and Middle Eastern Respiratory Syndrome (MERS), including viral pneumonia, fever, cough, chest discomfort, and in cases with severe illness, dyspnea and lung infiltrate (Hu et al., 2021).

The first recorded case of COVID-19 in Wuhan was dated back to December 8, 2020 (Hu et al., 2021); however, a recent WHO investigation found that mid-October to mid-November of 2019 as the plausible interval when the first case of SARS-CoV-2 emerged in Hubei province (Pekar, Worobey, Moshiri, Scheffler, & Wertheim, 2021).

2.1 SARS-CoV-2

SARS-CoV-2 is a member of the *Sarbecovirus*, a subgenus of *Betacoronaviruses* (β -coronavirus), which are found in horseshoe bats belonging to the family *Rhinophilidae* (Coronaviridae Study Group of the International Committee on Taxonomy of, 2020). SARS-CoV-2 is 96% identical at a whole-genome level to bat coronavirus, RaTG13, found in *Rhinolophus affinis* (Dos Santos, 2020; Hu et al., 2021; Lytras, Hughes, Xia, Jiang, & Robertson, 2021; P. Zhou et al., 2020). RaTG13 is not the progenitor of SARS-CoV-2 because of two fundamental factors:

“the first factor is the difference in the genetic sequences of the spike protein (Friend & Stebbing, 2021). The SARS-CoV-2 spike protein has a high affinity, unlike RaTG13 for human angiotensin-converting enzyme 2 (ACE2), the protein used in viral attachment and entry. The second factor is based on estimated mutation rates, which indicate that RaTG13 and SARS-CoV-2 share a common ancestor between 25 to 65 years ago; a timeline that does not work with the novel emergence of SARS-CoV-2 and its initial low genetic diversity” (Cohen, 2020).

An intermediate species exists which preceded the “spillover” event to humans; however, at this time, the intermediate species is not known. Discovery of the intermediate species is a difficult task, partly because RaTG13 was cultured in Yunnan Province, which is over 1500 km from Wuhan, where SARS-CoV-2 was first identified (P. Zhou et al., 2020).

2.1.1 Basic Virology

SARS-CoV-2 has a viral envelope coated by a spike glycoprotein (S protein), an envelope (E protein), and membrane (M) proteins (Cevik et al., 2020), as illustrated in Figure 1 below. SARS-CoV-2 is a positive-sense, single-stranded RNA virus with a genome that encodes 29 proteins (Dos Santos, 2020) and contains the capability to proofread during replication (Cevik et al., 2020). The S protein contains a highly variable receptor binding domain (RBD) (Dos Santos, 2020) which binds with high affinity to the peptidase domain of ACE2 (Cevik et al., 2020), followed by priming with a cellular serine protease (e.g. TMPRSS2) (Gupta et al., 2020), thereby facilitating the entry of the virus via membrane fusion.

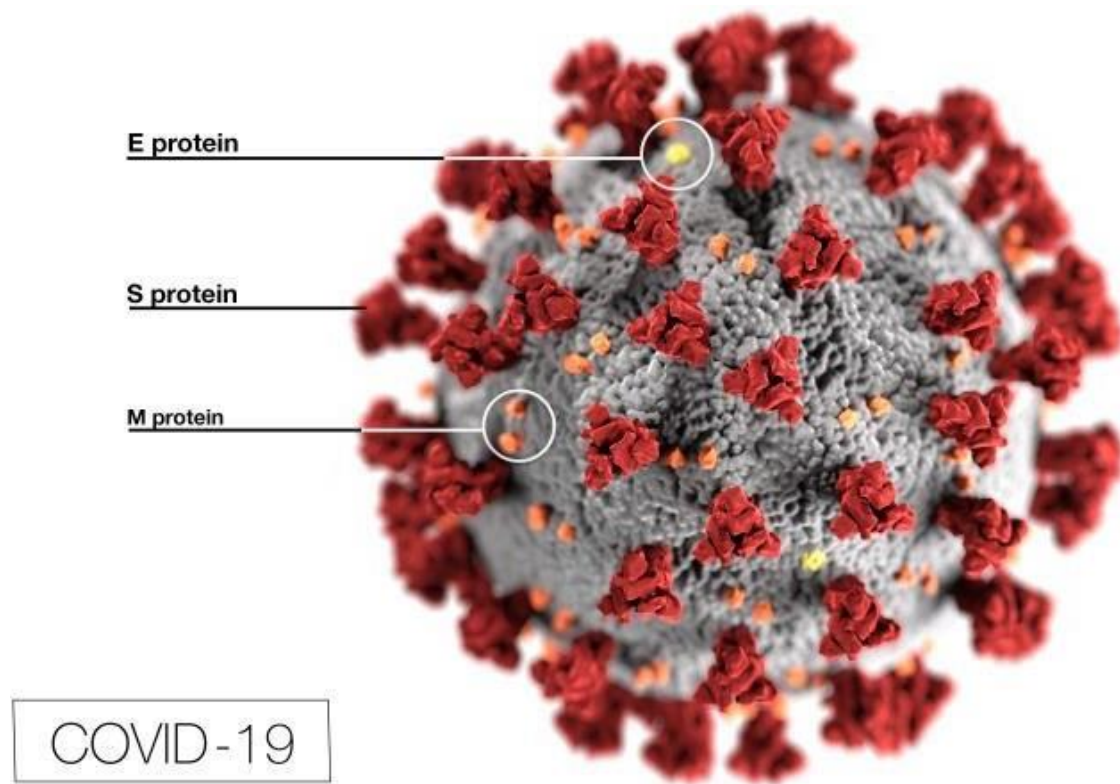


Figure 1 SARS-CoV-2 Illustration. The illustration reveals ultrastructural morphology exhibited by coronaviruses. Coronaviruses get their name due to the spikes which adorn the viral envelope, conveying the look of a corona that surrounds the virion when viewed through an electron microscope. Image is public domain (CDC, 2020b). *Image courtesy of content providers Alissa Eckert and Dan Higgins.*

2.1.2 Transmission Dynamics

SARS-CoV-2 is primarily transmitted via air, and infection occurs by direct or indirect contact of nasal, conjunctival, or oral mucosa with infected respiratory droplets (Cevik et al., 2020). Evidence suggests that SARS-CoV-2 can spread through aerosols, however, proximity is considered the key determinant of transmission (Meyerowitz et al., 2021). Evidence supporting

the role of fecal shedding and fomites in SARS-CoV-2 transmission are still not fully understood (Cevik et al., 2020; Meyerowitz et al., 2021).

Transmission of SARS-CoV-2 can occur through pre-symptomatic (one to two days before clinical manifestations), symptomatic, and asymptomatic spread (Cevik et al., 2020). Asymptomatic individuals appear less likely to transmit the virus, but it is not known when they are most infectious because data on the dynamics of viral shedding in asymptomatic cases is not well understood (Meyerowitz et al., 2021). With symptomatic cases, peak viral load in the respiratory tract occurs within a day of symptom onset (Cevik et al., 2020; Lauer et al., 2020; P. Zhou et al., 2020), with rapid decline thereafter. Replication competent virus in immunocompetent patients with mild to moderate disease has not been found after 10 days following symptom onset (Singanayagam et al., 2020; Wolfel et al., 2020).

SARS-CoV-2's ability to spread prior to symptoms, during the first week of illness, and to a lesser extent, asymptotically, have been major contributors to its global spread. For SARS-CoV-2, Petersen et al. estimated an R_0 of approximately 2.5, which means that for every index case, an average of 2.5 individuals are infected (2020). It should be noted that the R_0 for SARS-CoV-2 is hard to estimate based on the large number of undiagnosed cases – new strains, such as the B.1.1.7 lineage, a recently emerged strain, has a higher R_0 compared to pre-existing variants (Davies et al., 2021). Mounting evidence suggests that a majority of SARS-CoV-2 infections are the result of “super spreading” events, typically occurring indoors, where air flow and the air exchange rate are decreased (Meyerowitz et al., 2021).

2.2 COVID-19

Manifestation of SARS-CoV-2 infection, COVID-19, ranges from asymptomatic disease to severe respiratory failure with a high proportion of cases experiencing mild disease (Hu et al., 2021). One COVID-19 study performed in China analyzed over 72,000 cases, finding that approximately 81% of COVID-19 cases were asymptomatic or mild, approximately 14% of cases were severe and 5% of cases were critical, leading to possible death (Hu et al., 2021).

SARS-CoV-2 infection results in a diverse range of clinical manifestations throughout the body, with hematologic, cardiovascular, hepatobiliary, endocrinologic, neurologic, dermatologic, ophthalmologic, respiratory, renal, and gastrointestinal systems affected (Gupta et al., 2020); clinical manifestations of COVID-19 are illustrated in Figure 2. Key mechanisms in the role of COVID-19 pathophysiology include endothelial cell damage and thromboinflammation, dysregulation of the renin-angiotensin-aldosterone system (RAAS), dysregulation of the immune response, and direct viral toxicity (Gupta et al., 2020).

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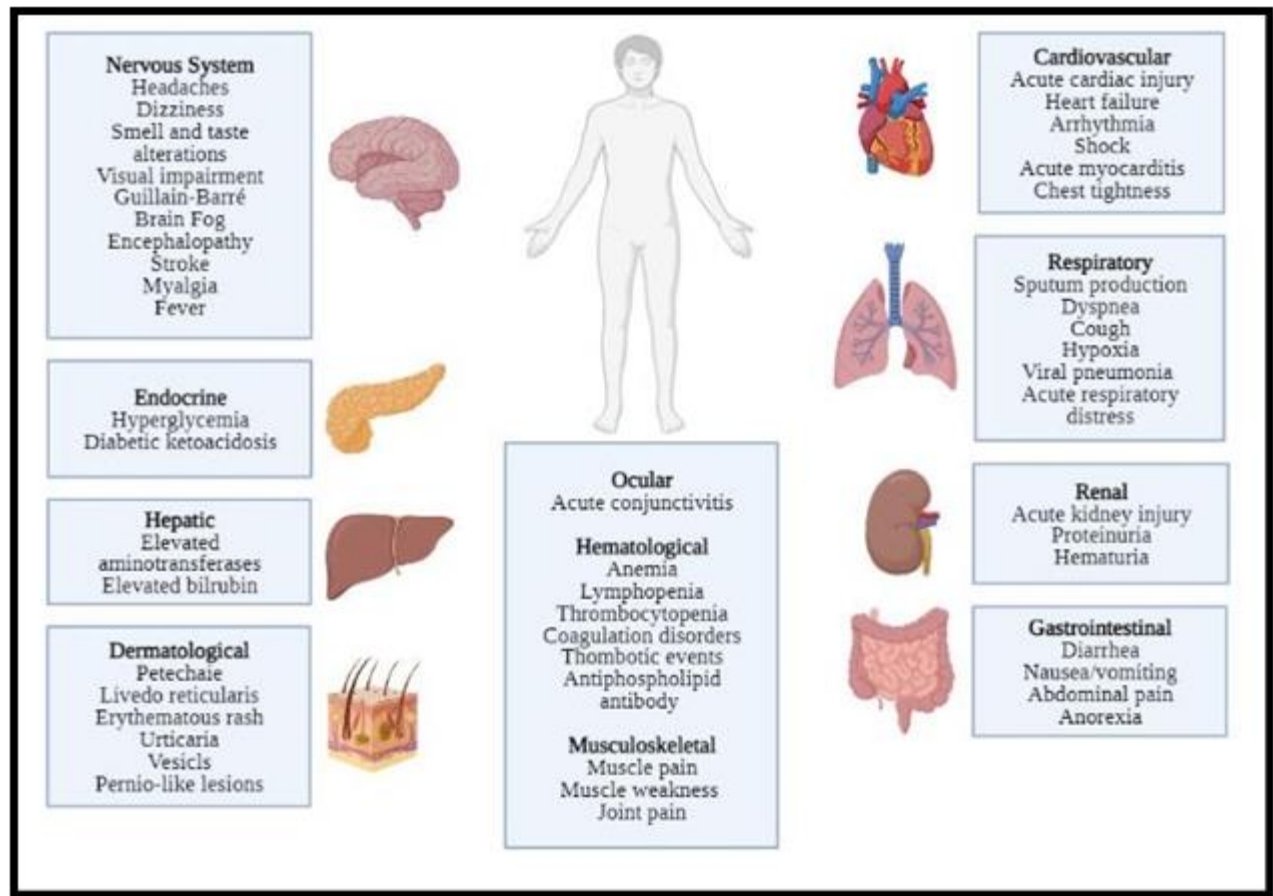


Figure 2 Summary of Systemic Manifestations of COVID-19. Illustrated is a summary of symptoms that manifest in each organ system because of SARS-CoV-2 infection (Gupta et al., 2020; Temgoua et al., 2020). This figure was created with BioRender.com by Cameron Green.

High risk factors for severe disease include old age (> 65 years of age), male sex, low SES, and pre-existing conditions, listed in Table 1 (Atkins et al., 2020; Barnett et al., 2012; CDC, 2021b; Cevik et al., 2020; Karmakar et al., 2021; Seligman et al., 2021; Williamson et al., 2020). Viral dynamics, such as high viral load kinetics, has also been shown to be a factor for determining disease severity and outcome (Cevik et al., 2020).

Table 1 Comorbidities Associated with Development of Severe Disease. The table is based on the CDC table of comorbidities and the level of risk they have for COVID-19 disease severity (CDC, 2020a).

Risk Level	Comorbidities
Increased Risk	Cancer Chronic Kidney Disease Chronic obstructive pulmonary disorder Down Syndrome Heart Conditions Obesity ($BMI \geq 30 \text{ kg/m}^2$) Severe Obesity ($BMI \geq 40 \text{ kg/m}^2$) Immunocompromised State Pregnancy Sickle Cell Disease Smoking Type 2 Diabetes Mellitus
May be at an Increased Risk	Asthma (moderate-to-severe) Cerebrovascular Disease Cystic Fibrosis Hypertension Dementia Liver Disease Overweight ($25 \text{ kg/m}^2 > BMI < 30 \text{ kg/m}^2$) Pulmonary Fibrosis Thalassemia Type 1 Diabetes Mellitus

3.0 The Role of Risk Factors and Comorbidities in COVID-19

Age is one of the greatest risk factors for severe COVID-19 illness (CDC, 2021b; Mallapaty, 2020), with 8 out of 10 COVID-19 deaths in the United States reported in adults older than 65 years of age (CDC, 2021b). In the United Kingdom (UK), by May 6th, 2020, over 90% of COVID-19 related deaths had occurred among individuals greater than 60 years of age (Strangfeld et al., 2021). Pre-existing conditions, such as cardiovascular disease, hypertension, diabetes, cancers, and obesity, have also been associated with an increased risk of severe disease and death (Atkins et al., 2020; Ejaz et al., 2020; Harrison, Fazio-Eynullayeva, Lane, Underhill, & Lip, 2020; Ssentongo, Ssentongo, Heilbrunn, Ba, & Chinchilli, 2020; Strangfeld et al., 2021). In addition, male sex and low SES have also been associated with increased COVID-19 incidence and mortality (Karmakar et al., 2021; Mallapaty, 2020; Williamson et al., 2020).

Advanced age is a significant risk factor for severe COVID-19 illness because of a higher rate of comorbidities (Barnett et al., 2012) and increased immune dysfunction (Callender et al., 2020). Immune dysfunction in advanced age consists of lower lymphocyte counts, increased pro-inflammatory cytokine levels, immunosenescence, and chronic low-grade inflammation (Callender et al., 2020; Mallapaty, 2020).

Comorbidities can hinder the body's ability to adequately respond in a stressful event, such as a viral infection. The comorbidities that impair the immune system and are known risk factors for severe COVID-19 include cancer, asthma, HIV, obesity, and diabetes (Ejaz et al., 2020). Diabetes, for example, which is one of the most prevalent pre-existing conditions documented in COVID-19 patients (Fadini, Morieri, Longato, & Avogaro, 2020; Guan, Liang, He, & Zhong,

2020; Yang et al., 2020; F. Zhou et al., 2020), impairs T-cell function and increases the production of IL-6, a pro-inflammatory cytokine (Ejaz et al., 2020). Beyond hindering immune system function, some comorbidities have been shown to upregulate ACE2 expression, which increases host cell susceptibility to viral invasion – these comorbidities, which are prevalent in patients with severe COVID-19, include hypertension, chronic obstructive pulmonary disorder (COPD), hepatic disease, renal disease, and diabetes (Ejaz et al., 2020).

Male biological sex, race/ethnicity, and low SES have also been related to poor COVID-19 prognosis (Callender et al., 2020). The dominant hypothesis for explaining the difference between sex is that females, with higher levels of estrogen, are more protected against severe COVID-19 because estrogen inhibits the activity or expression of RAAS and speeds the activation of the immune system (Gagliardi, Tieri, Ortona, & Ruggieri, 2020). The hypothesis for explaining race/ethnicity and low SES is due to underlying disparities. Minority populations and individuals of low SES are more likely to be exposed to SARS-CoV-2 because of crowded housing, an increased reliance on public transportation, and an increased possibility of working in essential front-line jobs (Karmakar et al., 2021).

4.0 Years of Life Lost

YLL models estimate the average number of years an individual would have lived had they not died due to a specified condition. YLL measurements use the age at which death occurs, placing greater weight on deaths at younger ages compared to more advanced age (Gardner & Sanborn, 1990; PHAST, 2020). The traditional process for measuring YLL is using age of death combined with life expectancy for a given age to estimate a weighted average of the years of life prematurely lost (Hanlon, 2021).

The equation for the total YLL is:

$$YLL = \sum[(d_i)(a_i)],$$

where ‘ d_i ’ is the number of observed deaths in the target population between ages 1 to x and ‘ a_i ’ is the difference between the LE for that age (x) to the age at death (Gardner & Sanborn, 1990; PHAST, 2020). Standard life tables are used for determining the LE of specific ages or age groups in a population or sub-population -- an example being actual life tables from the Social Security Administration.

4.1 Limitations for Years of Life Lost

YLL measurements tend to utilize standard life tables at the national or state level, which ignores the fact that LE can differ at significant levels depending on the neighborhood an individual resides in (Bilal et al., 2021; Chetty et al., 2016). Devleesschauwer (2016) posited another issue concerning life tables, specifically that a paradox may arise during a period of increased mortality risk, such as a pandemic, which may reduce LE, thus resulting in an underestimate of YLL.

YLL measurements vary on the type of life table or reference population chosen, and on the distribution of the ages of those who have passed from the condition. Furthermore, the accuracy of YLL measurements depend on the quality and completeness of data, and in the case of COVID-19, results are sensitive to public health mitigation strategies, medical treatments, and changes in viral transmission dynamics (Hanlon, 2021). Regardless, YLL provides public health officials and researchers a means to illustrate the severity a condition has upon society and within groups of a population.

5.0 Methods and Results

Articles on YLL due to COVID-19 related death were obtained primarily from PubMed. Articles were included in EndNote if they involved YLL for COVID-19 related deaths on any population. If an article obtained from PubMed cited a previous article which measured YLL due to COVID-19 related death, then that article was also included. The EndNote database generated was divided between YLL articles that included comorbidity in the measurements and those that did not.

5.1 Search Results

A total of 10 articles that focused on COVID-19 YLL were located and the overview for each article can be found in Table 2. Many of the articles ended data analysis during the spring or summer of 2020. Most of the literature measured YLL at the national level, with the United States being included more than any other country. There were two exceptions, one of which, by Mallow (2021), measured YLL in Ohio and calculated the economic loss of COVID-19. The second exception, by Pierce et al. (2021), measured YLL between different neighborhoods in Chicago, Illinois.

One piece of literature, by Hanlon et al., was assessed and found to include comorbidities in the measurement of YLL. Hanlon et al. estimated the likely combinations of comorbidities among people who died from COVID-19 up to the end of April 2020, then estimated YLL based

on life expectancy and single and multimorbidity combinations (Hanlon, 2021). The Hanlon et al. article is a manuscript which passed peer review as of March 1st, 2021.

Table 2 YLL Literature Overview. The table presents the YLL articles for COVID-19 that have been published, exist in pre-print or as a manuscript. The title, authors, a brief description of the article, and whether the article includes comorbidities are included in the table.

<i>Title</i>	<i>Description</i>	<i>Comorbidities</i>
<i>Potential Years of Life Lost Due to COVID-19 in the United States, Italy, and Germany: An Old Formula with Newer Ideas - (Mitra et al., 2020)</i>	Calculated YLL using 70, 75, and 80 as the upper age limits – data ends 30 May 2020.	No
<i>Years of Life Lost Attributable to COVID-19 in High-incidence Countries - (Oh et al., 2020)</i>	Calculated YLL in 30 high-incidence countries. Used the LE of a Japanese female – data ends 12 Jul 2020.	No
<i>Years of life lost associated with COVID-19 deaths in the United States - (Quast, Andel, Gregory, & Storch, 2020)</i>	YLL calculated by state using 2017 U.S. life tables – data ends 22 Jul 2020.	No
<i>COVID-19: How Many Years of Life Lost? - (Wetzler, Wetzler, & Cobb, 2020)</i>	YLL calculated in the U.S. using 2017 U.S. life tables – data ends 31 May 2020.	No
<i>2.5 Million Person-Years of Life Have Been Lost Due to COVID-19 in the United States - (Elledge, 2020)</i>	YLL calculated in the U.S. using 2017 U.S. life tables – data ends 3 Oct 2020.	No
<i>Estimates of the value of life lost from COVID-19 in Ohio - (Mallow, 2021)</i>	Builds upon the study listed above, but at the state level in Ohio, while also calculating the economic loss and YLL; uses 2017 U.S. life tables – data ends 30 Nov 2020.	No

6.0 Methods and Results

Accounting for comorbidities in YLL measurements is a difficult task. Analysis may require expensive computer simulations and complex statistical modelling and inference techniques, all of which are limiting factors for accessibility. Novel methods and techniques for the inclusion of comorbidities may have to be formulated, which takes time. Regardless, it is important to try to create a model or measurement that includes comorbidities, because adjusting for the presence of comorbidities can allow the public and health policy makers to better understand the burden of COVID-19 mortality.

Hanlon et al. used survival models based on comorbidity count, age, and sex, in combination with published data on patients who had died from COVID-19 in Italy and the United Kingdom (UK) to estimate YLL (Hanlon, 2021). The authors created a novel and replicable model to measure YLL while accounting for comorbidity, age, and sex.

Using the standard method of calculation of YLL (without comorbidities), Hanlon et al., estimated YLL early in the pandemic (up to the end of April), across all age groups in Italy, to be 14 YLL for males and 12 YLL for females (2021). Using aggregate data from Italy to account for 11 common comorbidities found in COVID-19 mortality, and life expectancy across all age groups in the UK, Hanlon et al. estimated men had 11.6 YLL and women had 9.4 YLL (Hanlon, 2021). The estimation of 14 YLL for men and 12 YLL for women, using the standard method of calculation, has been a fairly consistent estimation in literature throughout the pandemic, as Mallow, Elledge, Quast et al., Rommel et al., and Wetzler et al., each calculated similar YLLs (Elledge, 2020; Mallow, 2021; Quast et al., 2020; Rommel et al., 2021; Wetzler et al., 2020).

When Hanlon et al. examined the role of comorbidity count on age, they found that comorbidity count had a large impact on YLL (2021). For example, individuals at 70-79 years of age with zero comorbidities had 16.83 YLL, whereas those with five comorbidities had 3.60 YLL (Hanlon, 2021). Hanon et al. demonstrated that COVID-19 mortality with and without the presence of multimorbidity, represents a large burden of mortality.

There are several issues and limitations highlighted, which need to be corrected in future studies. The authors lacked individual-level data (i.e., health records), which likely resulted in a lack of information on comorbidity severity, a factor which impacts LE (Ioannidis, 2020). Hanlon et al. were also unable to adjust the model for factors and exposures associated with moderate to severe COVID-19, such as socio-economic status (SES), occupation, smoking, and weight (2021). Another limitation was the use of combined data on COVID-19 deaths and LE from different countries and contexts, which limits generalizability.

Despite the limitations, the authors were able to demonstrate, for the first time, that the number and type of comorbidity included in YLL measurements influence the estimated YLL compared to the standard approach. Their novel approach, based early in the pandemic, provides a promising framework for public health agencies, such as the CDC, to further develop the model.

6.1 Highlighting other Years of Life Lost Literature

Literature by Mallow and Pierce et al. are important for public health because they assess the impact of COVID-19 pre-mature mortality at the state level in Ohio and at the neighborhood level in

parts of Chicago. These were the first YLL articles discovered which estimate YLL at a level lower than the national level.

Mallow estimated COVID-19 YLL in Ohio, based on methods from Elledge (2020); however, Mallow went further and estimated the economic value from the lives lost. The inclusion of lost economic value from premature mortality is an effective public health tool for demonstrating the mortality impact of a condition and providing public health officials and policymakers key in to assess the risk-trade off from mitigation strategies.

Pierce et al. estimated YLL from COVID-19 in different neighborhoods in Chicago and illustrated the disparate impact COVID-19 has had and continues to have on racial/ethnic minorities and persons of low SES (Pierce et al., 2021). A study such as this is important because it highlights the need for targeted interventions to high-risk communities.

6.2 Next Steps

Future work should build upon the model put forth by Hanlon et al. by including personal-level data (i.e., personal medical records), additional clinical comorbidities, race, SES, occupation, specific health behaviors (e.g., tobacco smoking), and congregate setting status. Inclusion of these factors would provide a more definitive estimation of YLL. Furthermore, future research should also include the economic loss attributed to the premature deaths.

To ensure future research can occur, collaboration between governmental and academic institutions would be the most feasible option. Collaboration would allow researchers to access public records and if needed, access complex statistical computing software. It would also be

beneficial to strive for less-complex YLL models, which would increase accessibility for policy makers and clinical leaders in state and local institutions.

6.3 Public Health Implications

The inclusion of comorbidities in YLL models will result in the development of new prevention and treatment interventions to reduce COVID-19 complications and deaths. YLL models that include comorbidities could also be tailored to other diseases besides COVID-19. Inclusion of comorbidities would result in targeted policy development and public health interventions which could help to reduce morbidity and mortality.

Better representative YLL measurements provide more support behind public health communication efforts to ensure community members and policy makers understand the health risks and concerns relevant to at-risk groups. With greater understanding, individuals may be more likely to follow mitigation efforts to decrease morbidity and mortality in their community. Furthermore, YLL models with the inclusion of comorbidities could guide clinicians during times when resources are scarce (e.g., viral surge) by providing a reliable method for selecting the best candidates to receive the limited resources that are available.

7.0 Conclusion

YLL is an important public health tool because it allows clinicians and researchers to estimate the relative impact of a health condition on a population. The results of a YLL measurement or model can be used to guide policymaking and prioritization for interventions. YLL measurements are not perfect and are known to over-estimate YLL because individual-level factors, such as comorbidities, race, and SES are not normally included in the calculations.

COVID-19 disproportionately impacts the elderly, ethnic and minority populations, and those with certain pre-existing condition. It is essential these factors are included in YLL measurements to provide a more accurate representation of COVID-19 premature mortality. Hanlon et al. has provided an excellent framework of a YLL model which includes comorbidities. It is important to improve upon the model and continue analyzing the impact COVID-19 has on all populations, especially at-risk populations.

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